

This paper was presented at a colloquium entitled “Protecting Our Food Supply: The Value of Plant Genome Initiatives,” organized by Michael Freeling and Ronald L. Phillips, held June 2–5, 1997, sponsored by the National Academy of Sciences at the Arnold and Mabel Beckman Center in Irvine, CA.

Toward a successful multinational crop plant genome initiative

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ABSTRACT Plant genome research is needed as the foundation for an entirely new level of efficiency and success in the application of genetics and breeding to crop plants and products from crop plants. Genetic improvements in crop plants beyond current capabilities are needed to meet the growing world demand not only for more food, but also a greater diversity of food, higher-quality food, and safer food, produced on less land, while conserving soil, water, and genetic resources. Plant biology research, which is poised for dramatic advances, also depends fundamentally on plant genome research. The current *Arabidopsis* Genome Project has proved of immediate value to plant biology research, but a much greater effort is needed to ensure the full benefits of plant biology and especially plant genome research to agriculture. International cooperation is critical, both because genome projects are too large for any one country and the information forthcoming is of benefit to the world and not just the countries that do the work. Recent research on grass genomes has revealed that, because of extensive senteny and colinearity within linkage groups that make up the chromosomes, new information on the genome of one grass can be used to understand the genomes and predict the location of genes on chromosomes of the other grasses. Genome research applied to grasses as a group thereby can increase the efficiency and effectiveness of breeding for improvement of each member of this group, which includes wheat, corn, and rice, the world's three most important sources of food.

The world and especially the United States have benefited enormously during this century from a genetics approach to improving crops and livestock for agriculture. As an example, the United States grows at least 200 different crops, the great majority of which came originally as introductions from other countries, but then were manipulated genetically by using the tools of plant breeding to make them more suited to U.S. environments. These crops are more resistant to U.S. pests and diseases, and their products are more acceptable to U.S. consumers and foreign customers. As an example, the United States, Canada, and Mexico, working cooperatively, have kept the once devastating stem rust disease of wheat under control in the North American Great Plains for more than four decades—since the last serious epidemic in 1953—through strategic deployment of genes for resistance to stem rust in response to the ever-changing virulence in the pathogen population (1). Resistance has also been discovered and used in wheat to control stripe rust, the eyespot foot rot disease, Russian wheat aphid, greenbug, and Hessian fly. Resistance has been discovered and deployed in cotton for control of Fusarium and Verticillium wilts, thereby allowing the production of cotton on millions of acres in the southern and southwestern states where, otherwise, it would not be eco-

nomical to grow this crop. Likewise, with each of the other major crops and virtually every minor crop grown in the world, in addition to genetic improvements in yield and quality, genes for resistance to the diseases and pests of these crops have been identified and deployed, with great benefits to farmers, consumers, the environment, and society.

In spite of the progress and benefits, historically, conventional plant breeding based on classical genetics is a maturing technology. By itself, it may not continue to provide for world food needs, which are expected to double as the world population doubles over just the next 30–35 years. Genetic improvements in crop plants must be expanded, accelerated, and done much more precisely and efficiently to meet the growing world demand not only for more food, but also for a greater diversity of foods, higher-quality food, and safer food, produced on no more, and preferably less land, while protecting soil, water, and genetic resources. More extensive and rapid genetic improvements are also necessary in crops because of the large number of biotic and abiotic stresses for which crop plants with tolerance or resistance still must be developed, and because of the ability of pests and pathogens to rapidly adapt to each new crop or resistant variety, thereby perpetuating or increasing the dependency of agriculture on pesticides. Meeting these multiple goals and expectations will be possible only through greater application of the new tools of plant biotechnology. The efficient and rapid application of plant biotechnology, in turn, depends on plant genome research. Genome research applied to crop plants can take plant genetics and breeding to an entirely new level of efficiency and effectiveness on the road to further improvements in crops and the products from crops.

The Value of Plant Genome Research

The entire world became aware of both the practical and scientific value of genome research with the launching of the Human Genome Initiative, aimed at the development of a high-density physical map of the human genome through sequencing all of the approximately 70,000 genes and 3.3 billion bases of DNA. Equally important has been the basic research aimed at understanding the biological functions of human genes identified and sequenced, thereby helping to advance medical science. Although the goal remains focused on the human genome, several model organisms are under study as part of this large-scale sequencing project, including the insect *Drosophila melanogaster*, the nematode *Caenorhabditis elegans*, the yeast *Saccharomyces cerevisiae*, and the mouse *Mus musculus* (2). The fundamental and practical information revealed by this coordinated, multinational research effort makes clear that the quest for the knowledge contained in the genomes should be at the same level of priority scientifically as

the quest for the knowledge that can come from the exploration of any new frontier.

Plant biology research, which is poised for dramatic advances, also depends fundamentally on plant genome research. Unfortunately, plant genome research has lagged far behind human genome research. Only recently has this begun to change with the launching of the program to sequence the genome of the model plant *Arabidopsis thaliana*, estimated at up to 145 million bases. The project is now underway as a multinational effort, with the U.S. share funded by the National Science Foundation (NSF), U.S. Department of Agriculture (USDA), and the Department of Energy (DOE), with NSF as the lead agency. The *Arabidopsis* Genome Project has proved of immediate and critical value to plant biology research, but a much greater effort is needed to ensure the full benefits of plant biology and plant genome research to agriculture. Specifically, a greater effort is needed with crop plants, both to make full use of the information forthcoming from the *Arabidopsis* Genome Project and to provide critical information on crop plant genomes not likely to come from the *Arabidopsis* project.

Some of the practical benefits of the new knowledge and understanding that can come from this research when applied through the new tools of plant breeding are:

Accelerated improvements in the safety, quality, and diversity of food and other products of plants;

Greater assurance of food security worldwide in the face of a doubling of the world population over the next 30–35 years and declining agricultural land and quality water for irrigation;

Cleaner, healthier, environment and greater energy efficiency through improvements in fertilizer-use efficiency, thereby reducing production costs and concerns for ground-water contamination, and because of more sustainable disease and pest control through defenses delivered with seeds rather than with pesticides;

Expanded use of plant products, including higher-quality animal feeds, industrial feedstocks, and other value-added applications;

Continuation of the economic growth of the seed industry worldwide; and

Because of the expanded knowledge, further reduction in any potential environmental or human health risks that might arise with crop plants as a consequence of genetic modifications.

Knowledge of plant genomes is needed to expand the utility and value of crop plants beyond traditional uses. Thus, knowledge of genetic control of the biochemical pathways for synthesis of oil in plant seeds can greatly accelerate the development of crops as substitutes for petroleum-based products used for lubricants, plastics, and fuels (3). Increasingly, the world must shift from its current dependency on nonrenewable resources, such as fossil fuels, toward a greater dependency on renewable resources, such as can be provided by green plants grown as crops. Knowledge of the genetic control of biochemical pathways likewise can reveal approaches by which plants can be genetically modified specifically to meet the nutritional requirements for production of beef, pork, and poultry, thereby increasing the quality of these products and the efficiency of these industries. Similarly, control of protein profiles in grain to match the amino acid requirements of specific meat animals will make the grain more complete as feed, and further lower the cost of meat and milk production while lessening the amount of animal waste. Still other genetic modifications of plants can add value as biomedical products, including edible vaccines for humans (4) and animals (5).

Knowledge of plant genomes could also serve to reveal genetic vulnerabilities in plants currently troublesome as weeds. Some of the most important weeds are plants closely related to crop plants, and therefore their genomes are likely to be only slightly different from their crop plant relatives.

Knowledge of these differences, as well as similarities, in their plant genomes should help point to new approaches to weed control.

One of the greatest contributions of plant genome research will be to the seed industry. The development and marketing of new seeds, now valued at more than \$5 billion annually in the United States, has become a major growth industry worldwide. A public investment in plant genome research is needed as an underpinning to this industry where the information is available equitably to all companies, large and small, national and multinational. Knowledge of plant genomes is needed to sustain the seed industry as the foundation for sustainable growth of agriculture.

The Value of Genome Research Applied to Grasses

The grasses include the world's three most important sources of human food, namely wheat, corn, and rice. Worldwide production of these three crops for 1996–97 is estimated at 579 metric tons for wheat, 573 metric tons for corn, and 558 metric tons for rice. In addition, the grasses include barley, oats, sugarcane, sorghum, millets, and a large number of others representing important sources of calories and protein for human and animal consumption in different countries. Equally or more importantly, more than three-fourths of all cultivated land in the world is planted to grasses, including forage grasses grown for animal feed. Although grasses respond to irrigation, many members of this plant family as a group are well adapted to conditions of dry-land agriculture (e.g., sorghum, wheat, barley), including to agricultural areas with low rainfall and saline soils. Thus, any initiative with the goal of ensuring food security without clearing more land and with declining quality water for irrigation must give major attention to the grasses.

Recent research has revealed that, in spite of the diversity of grasses as a plant group, the genomes of grasses are remarkably similar as indicated by extensive conservation not only of genes but of entire linkage groups that make up the chromosomes (6, 7). The implication from this information is that research on the genome of one member of this group can be used to understand the genome and even predict the locations of genes on chromosomes of other members of this group. Genome research applied to grasses as a group therefore can greatly increase the efficiency and effectiveness of breeding for improvement of each member of the group.

Genomic research applied to grasses is also needed to complement and expand the knowledge base anticipated from the *Arabidopsis* Genome Project. Although a project that concentrates on this single seed-bearing plant is readily justified because of the high degree of conservation of genes across all families of seed plants and because of the small size of its genome, nevertheless, complete understanding of the genome of this one model plant will not explain the vast ecological, physiological, and morphological differences that exist among the economically important plants. An analysis only of the genome of *A. thaliana*, a dicot, will leave many unanswered questions about the genetic control of traits characteristic of wheat, corn, rice, other grasses, and other monocots. Any consideration for an increase in the investment in plant genome research aimed at development of high-density physical as well as genetic maps ideally should consider genome research applied to the grasses as the next area of emphasis beyond the current emphasis on *A. thaliana*.

On the other hand, just as understanding of the genome of one model plant may explain the similarities but not the differences among all crop plants, so genome research applied to a single grass plant may explain the similarities but not the differences among all economically important grass plants. As a minimum, genome research applied to grasses should proceed simultaneously and coordinately on wheat and barley as one group, corn and sorghum as a second group, and rice as

a third group, so as to provide maximal information on each of these unique and economically most important representatives of this plant group. The development of genetic maps and some sequencing work is already in progress for each of these three groups of crop plants representing the grasses. However, this effort could be better coordinated as a single collaborative, multinational, grass genome research project.

Role of the Public Investment in Plant Genome Research

A public investment in plant genome research is urgently needed to ensure that the information from plant genome research remains in the public domain, available to the public and private sectors alike. Without public funding, plant genome projects will be left to the private sector by default. Clearly, the private sector has much to gain from the information provided by plant genome research, including increasing their efficiency in variety and hybrid development and adding to their portfolio of intellectual property rights. However, this could further intensify vertical integration of the plant biotechnology industry, which is already a concern worldwide.

It is in the best interest of agriculture for the public and private sectors to work together. Some of the ways the public sector already aids the private sector in plant improvement programs in the United States include:

By making new plant material available through a national network of plant introduction stations;

Through maintenance of the nation's genetic resources in national seed banks and clonal repositories, ensuring that such resources remain in the public domain;

Through development of new and improved plant germplasm, which is then turned over to the private sector;

Through State Crop Improvement Associations under authority of the State Departments of Agriculture for the scale-up of new varieties;

Through maintenance of databases on genomes and genes, ensuring that the information within these databases remains within the public domain; and

Through investments in fundamental research, to expand the knowledge base and open new directions for applied research.

The Role of Multinational Cooperation

International cooperation is critical to the goals of genome research. Such projects are too large for any one country. Moreover, the world and not just the countries that do the work benefit from the information provided by these projects. Several models of multinational cooperation in plant genome research are available, including the International Triticeae Mapping Initiative (ITMI), the North American Barley Genome Mapping Project, and the above-mentioned *Arabidopsis* Genome project. Indeed, agricultural science has a long history of international cooperation.

Achieving a successful multinational, coordinated plant genome project depends on attention to a few general criteria required of any project where success depends on teamwork. Each member of the team, whether an individual, institution,

government agency, or nation, must bring certain skills, resources, and commitment to the team effort. Similarly, the team works best when each member has a clear understanding of their individual roles/obligations as well as the roles/obligations of every other member of the team, with minimal duplication or overlap except by design. Obviously, results must be shared readily and in a timely way. Most importantly, identity/visibility must be forthcoming to each team member, as determined by both their own specific contributions and the success of the project as a whole. If any one of these criteria is not met, the project likely will not succeed or will fall short of its potential.

The *Arabidopsis* Genome Project illustrates one approach to a multinational collaborative effort; the European Union, Japan, and the United States each agreed to sequence one or more of the five chromosomes that make up the genome of this plant. By this simple division of the workload based on a joint plan, each of the criteria outlined above for a successful team-driven project is or potentially can be met. The United States contribution to this project, in turn, is carried out as a single, coordinated, multiagency effort funded jointly by the NSF, USDA, and DOE, with NSF as the lead agency and providing most of the funds. These funds are awarded competitively to U.S. institutions where the work is done.

A multinational grass genome project could be initiated whereby different countries would agree to take the lead or share the lead in genomic research applied to one or more of the linkage groups common to grasses. Because of the extensive colinearity in grass genomes, it should be possible to identify these linkage groups and for the participating countries to then concentrate on researching these groups while working with the grass plant of their choice. Thus, a country or countries with interest primarily in rice could fulfill their role(s) in this collaborative effort by working with rice. Similarly, a country or countries with interest primarily in corn, or wheat, could fulfill their role(s) by working with corn or wheat. This approach provides for national identity/visibility and gives emphasis to grasses as a group, yet provides a mechanism for a single, multinational collaborative grass genome project. Such a project obviously should take advantage of existing multinational collaborative efforts in genetic mapping, such as those on wheat, barley, rice, and corn. The project logically would also allow for different levels of genomic research, with some concentrating on genetic mapping and others on high-density physical mapping. This approach would both minimize duplication and maximize the amount of information made available on grass genomes.

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